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FEB 08 2001 1647

TECH CENTER 1600/2000

ENTERED #27

C. Sack

RAW SEQUENCE LISTING DATE: 02/01/2001
 PATENT APPLICATION: US/08/765,588A TIME: 12:12:02

Input Set : A:\sequence.asc
 Output Set: N:\CRF3\02012001\H765588A.raw

4 <110> APPLICANT: Hayward, Nicholas K.
 5 Weber, Gunther
 6 Grimmond, Sean
 7 Nordenskjold, Magnus
 8 Larsson, Catharina
 10 <120> TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
 11 SAME
 13 <130> FILE REFERENCE: DAVIES
 15 <140> CURRENT APPLICATION NUMBER: 08/765,588A
 C--> 16 <141> CURRENT FILING DATE: 1997-04-27
 18 <160> NUMBER OF SEQ ID NOS: 22
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 649
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Nucleotide Sequence of VEGF165
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (17)..(589)
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 35 1 5 10
 37 gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100
 39 Ala Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
 40 15 20 25
 42 atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148
 44 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
 45 30 35 40
 47 gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196
 49 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
 50 45 50 55 60
 52 atc ttc cag gag tac ctc gat gag atc gag tac atc ttc aag cca tcc 244
 54 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
 55 65 70 75
 57 tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg 292
 59 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
 60 80 85 90
 62 gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg 340
 64 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
 65 95 100 105
 67 atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cay 388
 69 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
 70 110 115 120
 72 cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa 436
 74 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
 75 125 130 135 140

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79 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
80          145           150           155
82 gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc      532
84 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
85          160           165           170
87 aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag      580
89 Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
90          175           180           185
92 ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgttcgg            629
94 Pro Arg Arg
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97 gaaccagatc tctcaccagg
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102 <211> LENGTH: 191
103 <212> TYPE: PRT
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111          20          25          30
113 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
114          35          40          45
116 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
117          50          55          60
119 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
120          65          70          75          80
122 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
123          85          90          95
125 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
126          100         105         110
128 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
129          115         120         125
131 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
132          130         135         140
134 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
135          145         150         155         160
137 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
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146 <211> LENGTH: 1094
147 <212> TYPE: DNA
148 <213> ORGANISM: Nucleotide Sequence of SOM175
150 <220> FEATURE:
151 <221> NAME/KEY: CDS
152 <222> LOCATION: (3)..(623)

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 160 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 162 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 163 20 25 30
 165 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 167 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 168 35 40 45
 170 cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 172 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 173 50 55 60
 175 gtg gcc aaa cug ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 177 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 178 65 70 75
 180 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 182 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 183 80 85 90 95
 185 caa gtc cgg atg cag atc ctc atq atc cgg tac ccc agc aat cag ctg 335
 187 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
 188 100 105 110
 190 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
 192 Gly Glu Met Ser Leu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
 193 115 120 125
 195 aaa aag gac aat gct gtg aag cca gac agg gct gcc act ccc cac cac 431
 197 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
 198 130 135 140
 200 cgt ccc cag ccc cgt tct gtt ccc ggc tgg gac tct gcc ccc gga gca 479
 202 Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
 203 145 150 155
 205 ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527
 207 Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
 208 160 165 170 175
 210 gcc cac gct gca ccc agc acc acc agc ggc ctg acc ccc gga cct gcc 575
 212 Ala His Ala Ala Pro Ser Thr Ser Ala Leu Thr Pro Gly Pro Ala
 213 180 185 190
 215 gct gcc gct gcc gac gca gct tcc tcc gtt gcc aag ggc ggg gct 623
 217 Ala Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 218 195 200 205
 220 tagagctaa cccagacacc tgcaagggtgcc gggaaagctgccc aagggtgacac atggcttttc 683
 223 agactcagca gggtgacttg ctcagaggc tataatcccg tggggaaaca aagggggagcc 743
 226 tggtaaaaaa cagccaaagcc cccaaagacct cagccccggc agaaatgtctt ctaggacactg 803
 229 ggcctctcag agggctcttc tgccatccct tggctccctg agggccatcat caaacaggac 863
 232 agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct cagggggaaa 923
 235 tggatgttgc ttcagttt taaccactt gtgtcaagttaa gcatatttaca actggcttt 983
 238 ctcctccctca ctaagaagac ccaaaccctt gctataatggg atttgggtt tggtacaaga 1043
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 245 <210> SEQ ID NO: 4

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/08/765,588A DATE: 02/01/2001
 TIME: 12:12:02

Input Set : A:\sequence.asc
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248 <213> ORGANISM: Nucleotide Sequence of SOM175
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255     20          25          30
257 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
258     35          40          45
260 Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
261     50          55          60
263 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
264     65          70          75          80
266 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
267     85          90          95
269 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
270     100         105         110
272 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
273     115         120         125
275 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
276     130         135         140
278 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
279     145         150         155         160
281 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
282     165         170         175
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293 <211> LENGTH: 993
294 <212> TYPE: DNA
295 <213> ORGANISM: Nuc. Seq. of SOM175 Absent Exon 6
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298 <221> NAME/KEY: CDS
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309 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
310     20          25          30
312 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc     143
314 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
315     35          40          45
317 cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc     191
319 Gln Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr

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325	65					70							75				
327	ggc	tgc	tgc	cct	gac	gat	ggc	ctg	gag	tgt	gtg	ccc	act	ggg	cag	cac	287
329	Gly	Cys	Cys	Pro	Asp	Asp	Cys	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	
330	80				85				90							95	
332	caa	gtc	cgg	atg	cag	atc	ctc	atg	atc	egg	tac	ccg	agc	agt	cag	ctg	335
334	Gln	Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	
335						100			105				110				
337	ggg	gag	atg	tcc	ctg	gaa	gaa	cac	agc	cag	tgt	gaa	tgc	aga	cct	aaa	383
339	Gly	Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	
340						115			120				125				
342	aaa	aag	gac	agt	gct	gtg	aag	cca	gat	agc	ccc	agg	ccc	ctc	tgc	cca	431
344	Lys	Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Ser	Pro	Arg	Pro	Leu	Cys	Pro	
345						130			135			140					
347	cgc	tgc	acc	cag	cac	cac	cag	cgc	cct	gac	ccc	cgg	acc	tgc	cgc	tgc	479
349	Arg	Cys	Thr	Gln	His	His	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	
350						145			150			155					
352	cgc	tgc	cga	cgc	cgc	agc	ttc	ctc	cgt	tgc	caa	ggg	cgg	ggc	tta	gag	527
354	Arg	Cys	Arg	Arg	Arg	Ser	Phe	Ieu	Arg	Cys	Gln	Gly	Arg	Gly	Ieu	Glu	
355						160			165			170			175		
357	ctc	aac	cca	gac	acc	tgc	agg	tgc	cgg	aag	ctg	cga	agg	tgacacatgg		576	
359	Leu	Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg				
360						180			185								
362	ctttca	gac	tc	agc	agg	gt	gct	gg	gt	act	gc	c	tc	t	gg	aaagg	636
365	gg	ac	ct	gg	tt	gg	tt	gg	gg	gg	gg	gg	gg	gg	gg	gg	696
368	gac	ct	gg	gg	cc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	756
371	cagg	ac	ag	ag	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	816
374	gg	ga	at	tg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	876
377	gt	ct	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	936
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397						35			40			45					
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400						50			55			60					
402	Ala	Lys	Gln	Leu	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	
403						65			70			75			80		
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VERIFICATION SUMMARY DATE: 02/01/2001
PATENT APPLICATION: US/08/765,588A TIME: 12:12:03

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date